

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:38:08 ; Search time 57 Seconds  
(without alignments)  
7401.817 Million cell updates/sec

Title: US-10-090-183-6

Perfect score: 7046

Sequence: 1 MESKALLAVALWFCVETRAA.....KMWDAVAHADSGTTLRSPV 1345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications\_AA.\*

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7046	100.0	1345	14	US-10-090-183-6
2	7020	99.6	1367	9	US-09-766-678-2
3	7020	99.6	1367	15	US-10-165-193A-10
4	6994	99.3	1367	9	US-09-919-408-6
5	6994	99.3	1367	9	US-09-872-136-6
6	6127.5	87.0	1356	14	US-10-024-939-2
7	6127.5	87.0	1356	14	US-10-100-405A-2
8	6127.5	87.0	1356	14	US-10-327-414-6
9	6127.5	87.0	1356	15	US-10-165-193A-11
10	6124.5	86.9	1356	15	US-10-090-183-2
11	6124.5	86.9	1356	15	US-10-394-322A-66
12	6124.5	86.9	1356	15	US-10-440-464-129
13	6123.5	86.5	1356	10	US-09-969-037-7
14	6092.5	86.5	1354	14	US-10-262-538-30
15	4228	60.0	806	9	US-09-766-678-5

16	4196	59.6	805	13	US-10-036-869-34	Sequence 34, Appl
17	3851	54.7	731	14	US-10-364-949-2	Sequence 2, Appl
18	3343	47.4	789	14	US-10-101-018-15	Sequence 15, Appl
19	3283	46.6	773	14	US-10-364-949-4	Sequence 4, Appl
20	3245	46.1	767	14	US-10-105-901-2	Sequence 2, Appl
21	3240	46.0	764	14	US-10-091-300-85	Sequence 85, Appl
22	3143	44.6	942	16	US-10-449-609-8	Sequence 34, Appl
23	3126	44.4	738	14	US-10-425-668-34	Sequence 13, Appl
24	2792	39.6	664	14	US-10-101-018-13	Sequence 8, Appl
25	2764.5	39.2	567	14	US-10-327-414-8	Sequence 19, Appl
26	2746.5	39.0	1363	10	US-09-375-248-19	Sequence 19, Appl
27	2746.5	39.0	1363	12	US-10-661-740-19	Sequence 19, Appl
28	2733.5	38.8	1368	14	US-10-105-901-34	Sequence 215, Appl
29	2694.5	38.2	1338	12	US-10-211-462-215	Sequence 23, Appl
30	2694.5	38.2	1338	12	US-10-060-065-23	Sequence 44, Appl
31	2694.5	38.2	1338	14	US-10-059-585-44	Sequence 84, Appl
32	2694.5	38.2	1338	14	US-10-021-660-84	Sequence 26, Appl
33	2694.5	38.2	1338	16	US-10-621-116-26	Sequence 4, Appl
34	2692.5	38.2	1338	14	US-10-090-183-4	Sequence 129, Appl
35	2692.5	38.2	1338	15	US-10-116-275-129	Sequence 33, Appl
36	2691.5	38.2	1362	14	US-10-105-901-33	Sequence 2, Appl
37	2688	38.1	1339	15	US-10-165-193A-9	Sequence 2, Appl
38	2682	38.1	1363	10	US-09-375-248-2	Sequence 4, Appl
39	2682	38.1	1363	12	US-09-765-534B-4	Sequence 2, Appl
40	2682	38.1	1363	12	US-10-661-740-2	Sequence 33, Appl
41	2677.5	38.0	1298	9	US-09-982-610-33	Sequence 3, Appl
42	2677.5	38.0	1298	12	US-09-765-534B-2	Sequence 32, Appl
43	2677.5	38.0	1298	14	US-10-262-538-32	Sequence 67, Appl
44	2677.5	38.0	1298	15	US-10-394-322A-67	Sequence 5, Appl
45	2672.5	37.9	1311	12	US-09-765-534B-5	

#### ALIGNMENTS

RESULT 1  
US-10-090-183-6  
; Sequence 6, Application US/10090183  
; Publication No. US20030185802A1  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Ralph A. Reisfeld  
; APPLICANT: Andrew G. Niethammer  
; APPLICANT: Rong Xiang  
; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING  
; TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF  
; FILE REFERENCE: TSRI-829.0  
; CURRENT FILING DATE: 2002-03-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1345  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-090-183-6

Query Match 100.0%; Score 7046; DB 14; Length 1345;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MESKALLAVALWFCVETRAASVGLTGFHPKLSQDKDILTILANTTLQITCRGORDLD	60
DB	1	MESKALLAVALWFCVETRAASVGLTGFHPKLSQDKDILTILANTTLQITCRGORDLD	60
QY	61	WLWPNQARDSEERVLVTECGGDSIFCKTLTIPRVVGNDTGAYKCSYRDVDTASTVYVYV	120
DB	61	WLWPNQARDSEERVLVTECGGDSIFCKTLTIPRVVGNDTGAYKCSYRDVDTASTVYVYV	120
QY	121	RDYRSPFIASVDQHGIVITENKNTVIPCRCGISNLNLSLCARYPEKRPVPGNRTS	180
DB	121	RDYRSPFIASVDQHGIVITENKNTVIPCRCGISNLNLSLCARYPEKRPVPGNRTS	180

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:35:17 ; Search time 23 Seconds  
(without alignments)  
3018.997 Million cell updates/sec

Title: US-10-090-183-6

Perfect score: 7046

Sequence: 1 MESKALLAVALMFCVETRAA.....KMDAANVHDSGTTLRSPV 1345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7020	99.6	1367	2	US-08-443-861-2
2	7020	99.6	1367	3	US-08-193-829B-2
3	6994	99.3	1367	1	US-07-813-593-4
4	6994	99.3	1367	1	US-07-977-451-6
5	6994	99.3	1367	1	US-07-946-507-4
6	6994	99.3	1367	1	US-08-252-517-6
7	6994	99.3	1367	1	US-07-906-397A-6
8	6994	99.3	1367	1	US-08-601-891-6
9	6994	99.3	1367	2	US-09-021-324-6
10	6994	99.3	1367	4	US-09-872-132B-6
11	6994	99.3	1367	5	PCT-US92-02750-8
12	6994	99.3	1367	5	PCT-US92-05401-6
13	6994	99.3	1367	5	PCT-US92-09893-6
14	6127.5	87.0	1356	3	US-09-098-707A-2
15	6127.5	87.0	1356	4	US-09-483-539-2
16	6102.5	86.6	1356	1	US-08-810-116-8
17	6102.5	86.6	1356	2	US-07-930-548A-8
18	4228	60.0	806	2	US-08-443-861-5
19	4228	60.0	806	3	US-08-193-829B-5
20	4196	59.6	806	3	US-08-985-526-34
21	3327.5	47.2	788	1	US-08-232-538-15
22	3327.5	47.2	788	2	US-08-786-164-15
23	3248	46.1	764	4	US-09-142-956B-14
24	3245	46.1	767	2	US-08-874-678-2
25	3245	46.1	767	3	US-08-643-839-2
26	3245	46.1	767	4	US-09-348-886-2
27	2792	39.6	668	1	US-08-233-538-13

28	2792	39.6	668	2	US-08-786-164-13	Sequence 13, Appl
29	2733.5	38.8	1368	2	US-08-874-678-34	Sequence 34, Appl
30	2733.5	38.8	1368	3	US-08-643-839-34	Sequence 34, Appl
31	2733.5	38.8	1368	4	US-09-348-886-34	Sequence 34, Appl
32	2694.5	38.2	1338	3	US-08-750-141A-3	Sequence 3, Appl
33	2694.5	38.2	1338	4	US-09-119-014D-6	Sequence 6, Appl
34	2691.5	38.2	1362	2	US-08-874-678-33	Sequence 33, Appl
35	2691.5	38.2	1362	3	US-08-643-839-33	Sequence 33, Appl
36	2691.5	38.2	1362	4	US-09-348-886-33	Sequence 33, Appl
37	2682	38.1	1363	1	US-08-340-011-4	Sequence 4, Appl
38	2682	38.1	1363	3	US-08-901-710-4	Sequence 4, Appl
39	2677.5	38.0	1298	1	US-08-222-616-33	Sequence 33, Appl
40	2677.5	38.0	1298	1	US-08-340-011-2	Sequence 2, Appl
41	2677.5	38.0	1298	3	US-08-901-710-2	Sequence 33, Appl
42	2677.5	38.0	1298	4	US-08-446-648-33	Sequence 33, Appl
43	2677.5	38.0	1298	4	US-09-982-610-33	Sequence 33, Appl
44	2677.5	38.0	1298	5	PCT-US95-04228-33	Sequence 33, Appl
45	2672.5	37.9	1311	1	US-08-340-011-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-08-443-861-2  
; Sequence 2, Application US/08443861  
; Patent No. 5851999  
; GENERAL INFORMATION:  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Risau, Werner  
; APPLICANT: Millauer, Birgit  
; APPLICANT: Gazit, Aviv  
; APPLICANT: Levitzki, Alex  
; TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular  
; TITLE OF INVENTION: Endothelial Growth Factor  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,861  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/193,829  
; FILING DATE: 09-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-060  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)790-9090  
; TELEFAX: (212)869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1367 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-443-861-2  
Query Match 99.6%; Score 7020; DB 2; Length 1367;  
Best Local Similarity 99.9%; Pred. No. 0;

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:34:27 ; Search time 21 Seconds  
(without alignments)  
6160.838 Million cell updates/sec

Title: US-10-090-183-6

Perfect score: 7046

Sequence: 1 MESKALLAVALWFCVETRAA.....KMWDAVHADSGTILRSPPV 1345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6998	99.3	1367	2 A41228	protein-tyrosine k
2	6102.5	86.6	1356	2 JCI402	protein-tyrosine k
3	4810.5	68.3	1348	2 S1656	vascular endotheli
4	2913	41.3	1379	2 JCA954	vascular endotheli
5	2746.5	39.0	1363	2 I58375	protein-tyrosine k
6	2694.5	38.2	1338	2 S09982	protein-tyrosine k
7	2677.5	38.0	1298	2 A48999	protein-tyrosine k
8	2606	37.0	1336	2 I60598	Fit-1 tyrosine kin
9	2575	36.5	1333	2 I78875	receptor tyrosine
10	2524.5	35.8	1330	2 S49010	embryonic receptor
11	1162.5	16.5	1088	1 PRTGA	platelet-derived g
12	1162	16.5	1089	1 PFHUGA	platelet-derived g
13	1142	16.2	1089	1 S33727	platelet-derived g
14	1130.5	16.0	1087	2 I51552	platelet-derived g
15	1077.5	15.3	975	2 T30816	macrophage colony-
16	1049.5	14.9	1048	2 T30815	platelet-derived g
17	1043.5	14.8	960	1 JN0677	protein-tyrosine k
18	1019.5	14.5	976	1 TVHUKT	protein-tyrosine k
19	1019	14.5	978	1 A49814	protein-tyrosine k
20	1019	14.5	1106	1 PFHUGB	platelet-derived g
21	1016.5	14.4	975	1 TVWSKT	protein-tyrosine k
22	1009	14.3	977	2 I45877	protein-tyrosine k
23	1003	14.2	806	2 A35963	protein-tyrosine k
24	1000.5	14.2	1098	1 PWSRB	platelet-derived g
25	999.5	14.2	819	1 TVCHFG	fibroblast growth
26	994	14.1	980	1 TVCTMD	macrophage colony-
27	993.5	14.1	816	2 A49151	fibroblast growth
28	992	14.1	814	1 A39752	fibroblast growth
29	992	14.1	821	1 TVWSBK	fibroblast growth

30	990.5	14.1	972	1 TVHUMD	macrophage colony-
31	989.5	14.0	954	2 I51703	c-kit-related kina
32	989	14.0	822	2 I49289	fibroblast growth
33	985	14.0	822	1 TVHUGF	fibroblast growth
34	984	14.0	821	1 TVHUF2	fibroblast growth
35	984	14.0	832	2 JH0393	fibroblast growth
36	981	13.9	822	1 TVMSFG	fibroblast growth
37	980.5	13.9	941	1 TVMSVD	protein-tyrosine k
38	976.5	13.9	812	1 A36477	fibroblast growth
39	974.5	13.8	820	2 S17295	fibroblast growth
40	974.5	13.8	822	2 A45081	fibroblast growth
41	973.5	13.8	822	2 B54846	fibroblast growth
42	972.5	13.8	823	2 B35963	protein-tyrosine k
43	972	13.8	822	2 S29840	fibroblast growth
44	966.5	13.7	822	2 A41794	keratinocyte growt
45	962	13.7	729	2 A56795	fibroblast growth

#### ALIGNMENTS

##### RESULT 1

A41228

protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 04-Feb-2000  
C:Accession: A41228; A46065; I58365; S18832; S29991  
R:Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.  
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991  
A>Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitive  
A:Reference number: A41228; MUID:92020984; PMID:1717995  
A:Accession: A41228  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1367 <WAT>  
A:Cross-references: GB:X59397; NID:G50976; PIDN:CAA42040.1; PID:G50977  
R:Millauer, B.; Witzmann-Voos, S.; Schurch, H.; Martinez, R.; Moller, N.P.; Risau, W.;  
Cell 72, 835-846, 1993  
A>Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a major  
A:Reference number: A46065; MUID:93208880; PMID:7681362

Result

No. Score Query Match Length DB ID Description

Db 61 WLWPAQNRDSERVLVTECGGDSIPCKTLTIPRVVGNDTGAYKCSYRDVDIASTVYVV 120  
Qy 121 RYRPFPTASVDQHGIVITENKNTKTVIPCRGSIINLVSLCARYPEKRFVPGNRLS 180  
Db 121 RYRPFPTASVDQHGIVITENKNTKTVIPCRGSIINLVSLCARYPEKRFVPGNRLS 180  
Qy 181 WDSIEGFTLPYSYMSIYAGVAFCEAKINDETYQSIYIVVVGRIYDVVILSPHIELSA 240  
Db 181 WDSIEGFTLPYSYMSIYAGVAFCEAKINDETYQSIYIVVVGRIYDVVILSPHIELSA 240  
Qy 241 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPRGTVAKMFLSTLTIESVT 300  
Db 241 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPRGTVAKMFLSTLTIESVT 300  
Qy 301 KSDQGEYTCVASSGRIMKNNRFFVRVHTKPTAFGSGMSLVEATVGSQVRIPVKLSYP 360  
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Qy 361 APDIKWYRNGRPISNYTMVGDDELTIMEVTERDAGNYTVILTNPISEKQSHVSLVYN 420  
Db 361 APDIKWYRNGRPISNYTMVGDDELTIMEVTERDAGNYTVILTNPISEKQSHVSLVYN 420  
Qy 421 VPPQIGEKALISPMDSYQGTWQTLCTVYANPPLHHIQWYQLEBACSYRPGQTSFYAC 480  
Db 421 VPPQIGEKALISPMDSYQGTWQTLCTVYANPPLHHIQWYQLEBACSYRPGQTSFYAC 480  
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Db 481 KSWRHVEDFQGGNKIEVTNKOVALIEGKNKTVSTLVIQANVSALYKCAINKAGRGV 540  
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Db 541 ISFHVIRGPEITVQAAQTEQESVLLCTADNTFENLTWYKLSQATSVHMGESLTPV 600  
Qy 601 CKNLDAWLKMGTFMSNSTNDILIVAFONASLODQGDYVCSAQDKTKRGHCLVKQLIIL 660  
Db 601 CKNLDAWLKMGTFMSNSTNDILIVAFONASLODQGDYVCSAQDKTKRGHCLVKQLIIL 660  
Qy 661 ERWAPMITGNLENQTTIGETIEVTCPASGNPPTHTWPKDNELTVESGIVLRDGNRL 720  
Db 661 ERWAPMITGNLENQTTIGETIEVTCPASGNPPTHTWPKDNELTVESGIVLRDGNRL 720  
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Db 721 TIIRVRKEDEGLYTCAQCNVLGCARAEITLFIIEGAQKTNLEVIILVGTAVIAMFFMLLL 780  
Qy 781 VILVTVKRANEGELKTGYLSIVMDPDELPLDRCERLPLDYASKWBFPRDLKLGKPLGR 840  
Db 781 VILVTVKRANEGELKTGYLSIVMDPDELPLDRCERLPLDYASKWBFPRDLKLGKPLGR 840  
Qy 841 GAFQGVIEADAFGIDKTATCKTVAKMLKEGATHSEHRLMSLKITLIHGHILNVNLL 900  
Db 841 GAFQGVIEADAFGIDKTATCKTVAKMLKEGATHSEHRLMSLKITLIHGHILNVNLL 900  
Qy 901 GACTKPGGLWTVFCKFNSTYLRGKNEFPVYKSGARPROGKDYVYGLSVDLKRR 960  
Db 901 GACTKPGGLWTVFCKFNSTYLRGKNEFPVYKSGARPROGKDYVYGLSVDLKRR 960  
Qy 961 LPSITSSQSSAGSFVEEKSLSVDEEASBEELYKDFLTLEHLCYSFQVAKMEFLASR 1020  
Db 961 LPSITSSQSSAGSFVEEKSLSVDEEASBEELYKDFLTLEHLCYSFQVAKMEFLASR 1020  
Qy 1021 KCIHRLAARNILLSKNVKKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIDRVY 1080  
Db 1021 KCIHRLAARNILLSKNVKKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIDRVY 1080  
Qy 1081 TTQSDVMSFGVLWEIIFSLGASYPGVKIDEEFCRLKEGTRWRAPDYTPPENYQTMALD 1140  
Db 1081 TTQSDVMSFGVLWEIIFSLGASYPGVKIDEEFCRLKEGTRWRAPDYTPPENYQTMALD 1140  
Qy 1141 WHBDPNQRPFSBELVHGLNLLQANAQDQKQYIVLPMSETLSMEEDSGLSLTPSVSCM 1200  
Db 1141 WHBDPNQRPFSBELVHGLNLLQANAQDQKQYIVLPMSETLSMEEDSGLSLTPSVSCM 1200

Qy 1201 EEEVCDPKFYDNTAGISHYLQNSKRSPVSVKTFEDIPLEPEVKVIPDDSQTDSCM 1260  
Db 1201 EEEVCDPKFYDNTAGISHYLQNSKRSPVSVKTFEDIPLEPEVKVIPDDSQTDSCM 1260  
Qy 1261 VLASEELKTLDRNKLSPSFGGMPKSRRESVASGNSQTSQSGYHSDDDTDTTVYSSD 1320  
Db 1261 VLASEELKTLDRNKLSPSFGGMPKSRRESVASGNSQTSQSGYHSDDDTDTTVYSSD 1320  
Qy 1321 EAGLLKMDVDAVAHADSGTTLR 1341  
Db 1321 EAGLLKMDVDAVAHADSGTTLQ 1341  
RESULT 2  
JC1402  
protein-tyrosine kinase (EC 2.7.1.112) KDR - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 28-Aug-1998 #text\_change 04-Feb-2000  
C:Accession: JC1402; I58357  
R:Terminator, B.I.; Dougher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.; Armellino, D.C.; Goepf-  
Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992  
A:Title: Identification of the KDR tyrosine kinase as a receptor for vascular endothelial  
A:Reference number: JC1402; MUID:93038639; PMID:1417831  
A:Accession: JC1402  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-48, 'I', '50-616', 'E', '618-700', 'E', '702-748', 'F', '750-1263', 'I', '1265-1290', 'P', '1292-1  
A:Cross-references: EMBL:X61656; NID:931717  
R:Terminator, B.I.; Carrion, M.E.; Kovacs, E.; Rasmussen, B.A.; Eddy, R.L.; Shows, T.B.  
Oncogene 6, 1677-1683, 1991  
A:Title: Identification of a new endothelial cell growth factor receptor tyrosine kinase.  
A:Reference number: I58357; MUID:92019839; PMID:1656371  
A:Accession: I58357  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 3-1356 <TER2>  
A:Cross-references: GB:L04947; NID:9186674; PID:AAA59459.1; PID:9186675  
C:Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.  
C:Genetics:  
A:Gene: GDB:KDR  
A:Cross-references: GDB:127921; OMIM:191306  
A:Map position: 4q12-q12  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kin  
F:766-790/Domain: transmembrane #status predicted <TM>  
F:832-1167/Domain: protein kinase homology <KIN>  
F:840-848/Region: protein kinase ATP-binding motif

Query Match 86.6%; Score 6102.5; DB 2; Length 1356;  
Best Local Similarity 85.4%; Pred. No. 2.1e-262;  
Matches 1160; Conservative 72; Mismatches 111; Indels 15; Gaps 3;

Qy 1 MESKALLAVALMFCVETRAASVGLTGDFLHPPKLSQKDLITLANTLTQITCRGORDLD 60  
Db 1 MESKALLAVALMFCVETRAASVGLTGDFLHPPKLSQKDLITLANTLTQITCRGORDLD 60  
Qy 61 WLWPAQNRDSERVLVTECGGDSIPCKTLTIPRVVGNDTGAYKCSYRDVDIASTVYVV 120  
Db 61 WLWPAQNRDSERVLVTECGGDSIPCKTLTIPRVVGNDTGAYKCSYRDVDIASTVYVV 118  
Qy 121 RYRPFPTASVDQHGIVITENKNTKTVIPCRGSIINLVSLCARYPEKRFVPGNRLS 180  
Db 119 RYRPFPTASVDQHGIVITENKNTKTVIPCRGSIINLVSLCARYPEKRFVPGNRLS 178  
Qy 181 WDSIEGFTLPYSYMSIYAGVAFCEAKINDETYQSIYIVVVGRIYDVVILSPHIELSA 240  
Db 179 WDSIEGFTLPYSYMSIYAGVAFCEAKINDETYQSIYIVVVGRIYDVVILSPHIELSA 238  
Qy 241 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPRGTVAKMFLSTLTIESVT 300  
Db 239 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPRGTVAKMFLSTLTIESVT 298

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:30:17 ; Search time 61 Seconds  
(without alignments)  
6229.941 Million cell updates/sec

Title: US-10-090-183-6  
Perfect score: 7046  
Sequence: 1 MESKALLAVALWFCVETRAA.....KWDAAVHADSGTILRSPV 1345

Scoring table: BLOSUMP62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	7046	100.0	1345	7	ABM79009	Abm79009 Murine Flk
2	7020	99.6	1367	6	ABR40197	Abr40197 Murine va
3	6994	99.3	1367	2	AAR31377	Aar31377 Human flk
4	6994	99.3	1367	2	AAR37504	Aar37504 Murine fl
5	6994	99.3	1367	2	AAR44996	Aar44996 Murine fl
6	6994	99.3	1367	2	AAR67537	Aar67537 Mouse flk
7	6994	99.3	1367	2	AAR97420	Aar97420 Murine fo
8	6994	99.3	1367	2	AAR19875	Aar19875 Murine fl
9	6994	99.3	1367	2	AAY08618	Aay08618 Murine fl
10	6994	99.3	1367	5	ABG70917	Abg70917 Mouse rec
11	6994	99.3	1367	5	AAE25820	Aae25820 Murine re
12	6991	99.2	1367	2	AAR28041	Aar28041 Flk-1. 3/
13	6988	99.2	1367	2	AAR67817	Aar67817 Flk1 rece
14	6980	99.1	1367	2	AAR54046	Aar54046 Sequence
15	6967.5	98.9	1373	4	AAV97782	Aay97782 Mouse Flk
16	6127.5	87.0	1356	4	AAV97783	Aay97783 Human KDR
17	6124.5	86.9	1356	4	AAE62475	Aab62475 Human VEG
18	6124.5	86.9	1356	4	AAR97576	Aay97576 Human Flk
19	6124.5	86.9	1356	6	ABR40196	Abr40196 Human vas
20	6124.5	86.9	1356	7	ADBO8954	Adbo8954 Human VEG
21	6124.5	86.9	1356	7	ABM79007	Abm79007 Human VEG
22	6123.5	86.9	1356	5	AAU79426	Aau79426 Human Kin
23	6119.5	86.9	1355	2	AAR80997	Aaw80997 Human rec
24	6119.5	86.9	1356	5	AAU79427	Aau79427 Human Kin
25	6119.5	86.9	1356	5	AAU79430	Aau79430 Human Kin

26	6119.5	86.9	1356	5	AAU79429	Aau79429 Human Kin
27	6102.5	86.6	1356	2	AAR26999	Aar26999 Novel typ
28	6102.5	86.6	1356	2	AAW59275	Aaw59275 Human KDR
29	4196	59.6	805	2	AAV06196	Aay06196 Anti-angi
30	3851	54.7	731	7	ADB80300	Adb80300 Soluble F
31	3568	50.6	848	2	AAW38240	Aaw38240 VEGF rece
32	3343	47.4	789	2	AAE62488	Aae62488 Truncated
33	3343	47.4	789	2	AAW68007	Aaw68007 Human sol
34	3327.5	47.2	788	2	AAW47038	Aaw47038 Soluble t
35	3283	46.6	773	7	ADB80302	Adb80302 Soluble h
36	3248	46.1	764	2	AAW69679	Aaw69679 KDR prote
37	3240	46.0	764	5	AAE28915	Aae28915 Human pro
38	3240	46.0	764	6	ABJ26808	Abj26808 VEGF bind
39	3240	46.0	764	7	ADD24478	Add24478 Human ant
40	3240	46.0	764	7	ADD80855	Add80855 Human KDR
41	3233.5	45.9	927	4	AAV97653	Aay97653 Flk-1extr
42	3225	45.8	760	4	AAE62477	Aae62477 Human VEG
43	3126	44.4	738	3	AAV29639	Aay29639 Human vas
44	3126	44.4	738	3	AAV59302	Aay59302 Human VEG
45	2792	39.6	664	2	AAE62486	Aae62486 Human svE

ALIGNMENTS

RESULT 1

ABM79009  
ID ABM79009 standard; protein; 1345 AA.

XX AC ABM79009;

XX DT 15-JAN-2004 (first entry)

XX DE Murine Flk-1.

XX KW Mouse; vascular endothelial growth factor; receptor; Flk-1; vaccine;  
genetic immunisation; gene therapy; cytostatic.

XX OS Mus sp.

XX PN WO2003073995-A2.

XX PD 12-SEP-2003.

XX PF 28-FEB-2003; 2003WO-US006256.

XX PR 02-MAR-2002; 2002US-00090183.

XX PA (SRI ) SCRIPPS RES INST.

XX PI Reisfeld RA, Niethammer AG, Xiang R;

XX DR WPI, 2003-756753/71.

XX DR N-PSDB; ACF80603.

XX PT New DNA vaccine for eliciting an immune response against proliferating  
endothelial cells comprising a DNA construct operably encoding a VEGF  
receptor protein in a carrier, useful for inhibiting tumor growth or  
angiogenesis.

XX PS Claim 3; Fig 6; 56pp; English.

XX CC The present sequence is the protein sequence of murine Flk-1, an  
endothelial growth factor receptor protein. A claimed DNA vaccine  
effective for eliciting an immune response against proliferating  
endothelial cells comprises a DNA construct operably encoding a VEGF  
receptor protein (e.g. Flk-1) in a carrier. The DNA construct may be a  
naked DNA construct or incorporated into a plasmid vector or into an  
attenuated bacterial vector such as attenuated Salmonella typhimurium.  
XX CC The DNA vaccine is used in claimed methods of inhibiting endothelial cell  
proliferation, inhibiting angiogenesis, and inhibiting tumour growth  
Sequence 1345 AA;

Query Match		100.0%; Score 7046; DB 7; Length 1345;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MESKALLAVALWFCVETRAASVGLTGDPLHPPKLSQKDIILTIANTLTQITCRGQDRLD 60
Db	1	MESKALLAVALWFCVETRAASVGLTGDPLHPPKLSQKDIILTIANTLTQITCRGQDRLD 60
Qy	61	WLWPNARDSEERVLVTECGGDSIFCKTLTI PRVGNNDTCAYKCSYRDVDIASTVYVY 120
Db	61	WLWPNARDSEERVLVTECGGDSIFCKTLTI PRVGNNDTCAYKCSYRDVDIASTVYVY 120
Qy	121	RDYRSPFIASVDQHGIVITENKNTVIFPCRGISINLNVSLCARYPEKEFVDPGNRIS 180
Db	121	RDYRSPFIASVDQHGIVITENKNTVIFPCRGISINLNVSLCARYPEKEFVDPGNRIS 180
Qy	181	WDSIGFTLPSYMSIYAGWFCBAKINDETQSIWYIVVVGRIYDVILSPPEHIELSA 240
Db	181	WDSIGFTLPSYMSIYAGWFCBAKINDETQSIWYIVVVGRIYDVILSPPEHIELSA 240
Qy	241	GEKLVNCTARTLNVLGDLFTWHSPPSKSHHKKIVNRDVKPFPCTVAKMFLSTLTIESVT 300
Db	241	GEKLVNCTARTLNVLGDLFTWHSPPSKSHHKKIVNRDVKPFPCTVAKMFLSTLTIESVT 300
Qy	301	KSDQGEYTCVASSGRMIRKNTFRVHTKPIAFSGMKSLVEATVGSQVRI PVKYLSP 360
Db	301	KSDQGEYTCVASSGRMIRKNTFRVHTKPIAFSGMKSLVEATVGSQVRI PVKYLSP 360
Qy	361	APDIKWYRNGRPIESNTYMI VGDDELTIMEVTERDAGNYTILTNPI SMEXQSHMVSIVN 420
Db	361	APDIKWYRNGRPIESNTYMI VGDDELTIMEVTERDAGNYTILTNPI SMEXQSHMVSIVN 420
Qy	421	VPOIGEKALISPNDSYQYGTMOQLTCTVYANPLPHIOMYQWLEBACSRPGQTSYAC 480
Db	421	VPOIGEKALISPNDSYQYGTMOQLTCTVYANPLPHIOMYQWLEBACSRPGQTSYAC 480
Qy	481	KEWRHVEDFOGKNIEYTKQYALIEGKNKTVSLVIOANVSALYKCEAINKAGRERV 540
Db	481	KEWRHVEDFOGKNIEYTKQYALIEGKNKTVSLVIOANVSALYKCEAINKAGRERV 540
Qy	541	ISFHVIRGPEITVQPAAPTEQESVSLCTADRNTFENLTWYKLSQATSVMHGESLTPV 600
Db	541	ISFHVIRGPEITVQPAAPTEQESVSLCTADRNTFENLTWYKLSQATSVMHGESLTPV 600
Qy	601	CKNLDAWLKNGTMSFNSNDILIVAFQNASLOQDGYVCSAQDKTKGRHCLVKQLIIL 660
Db	601	CKNLDAWLKNGTMSFNSNDILIVAFQNASLOQDGYVCSAQDKTKGRHCLVKQLIIL 660
Qy	661	ERMAPMITGNLENQTTIGETIEVTCPASGNPTPHITWFKDNETLVDSGIVLRDGNRNL 720
Db	661	ERMAPMITGNLENQTTIGETIEVTCPASGNPTPHITWFKDNETLVDSGIVLRDGNRNL 720
Qy	721	TIRVRKEDGGLYTCQACNVLCARAEFLIEGAQKTNLEVIILVGTAVIAMFFWLL 780
Db	721	TIRVRKEDGGLYTCQACNVLCARAEFLIEGAQKTNLEVIILVGTAVIAMFFWLL 780
Qy	781	VIVLRTVKRANEGELTKYLSIVMDPELDERCERLPYDASKWPEPRDLKGLPLGR 840
Db	781	VIVLRTVKRANEGELTKYLSIVMDPELDERCERLPYDASKWPEPRDLKGLPLGR 840
Qy	841	GAFQVTEADAFGDKTATCKTAVKMLKEGATHSEHRLMSELKILIHIGHNLVNLL 900
Db	841	GAFQVTEADAFGDKTATCKTAVKMLKEGATHSEHRLMSELKILIHIGHNLVNLL 900
Qy	901	GACTKPGGLMWIVFECKFNGNLSTYLGKNEFVPYKSGARFQGDYVYVGLSVDLKRR 960
Db	901	GACTKPGGLMWIVFECKFNGNLSTYLGKNEFVPYKSGARFQGDYVYVGLSVDLKRR 960
Qy	961	LDSITSSQSSASSGFVEEKSLSDVBEAESEELYKDFLTLEHLCYSFQVAKGMEFLASR 1020
Db	961	LDSITSSQSSASSGFVEEKSLSDVBEAESEELYKDFLTLEHLCYSFQVAKGMEFLASR 1020

Qy	1021	KCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVY 1080
Db	1021	KCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVY 1080
Qy	1081	TIQSDVMSFGVLLWEIFSLGASYPGVKIDEEFCRLKKEGTRMRAPDYTTPEMYQTMLDC 1140
Db	1081	TIQSDVMSFGVLLWEIFSLGASYPGVKIDEEFCRLKKEGTRMRAPDYTTPEMYQTMLDC 1140
Qy	1141	WHEDPNORPSFSELVEHLGNLLOANAQDQKQIVILPMSSETLSWEEDSGLSLPTSPVSCM 1200
Db	1141	WHEDPNORPSFSELVEHLGNLLOANAQDQKQIVILPMSSETLSWEEDSGLSLPTSPVSCM 1200
Qy	1201	EEEEVCDCPKFHYDNTAGISHYLQNSKRSPVSVKTFEDIPLPEPEVKVIPDSDSQTDSGM 1260
Db	1201	EEEEVCDCPKFHYDNTAGISHYLQNSKRSPVSVKTFEDIPLPEPEVKVIPDSDSQTDSGM 1260
Qy	1261	VLASELKTLEDNRNKLSPSFGGMPPSKRESVASEGNSQTSQYQSGVHSDDTDTTVYSSD 1320
Db	1261	VLASELKTLEDNRNKLSPSFGGMPPSKRESVASEGNSQTSQYQSGVHSDDTDTTVYSSD 1320
Qy	1321	EAGLLKMWDAAVHADSGTTLRSPPV 1345
Db	1321	EAGLLKMWDAAVHADSGTTLRSPPV 1345
RESULT 2		
ABR40197		
ID	ABR40197 standard; protein; 1367 AA.	
XX	ABR40197;	
AC	AC	
XX	01-AUG-2003 (first entry)	
DE	Murine vascular endothelial growth factor receptor-2.	
XX	Murine; vascular endothelial growth factor receptor-2; cytostatic;	
KW	angiogenic; antiangiogenic; antiarthritic; antirheumatic; antisense;	
KW	VEGFR-2; hyperproliferative disorder; cancer; rheumatoid arthritis;	
KW	angiogenesis.	
OS	Mus musculus.	
XX	WO2003029266-A1.	
PN	10-APR-2003.	
PD	26-SEP-2002; 2002WO-US030734.	
XX	28-SEP-2001; 2001US-00967655.	
XX	(ISIS-) ISIS PHARM INC.	
PA	Bennett CF, Watt AT;	
PI	WPI; 2003-371980/35.	
DR	N-PSDB; ACC71720.	
XX	New compounds, particularly antisense oligonucleotides targeted to a	
PT	nucleic acid encoding vascular endothelial growth factor receptor-2	
PT	(VEGFR-2), useful for treating a disease/condition associated with VEGFR-	
PT	2, e.g. cancer.	
XX	Example 13; Page 99-105; 127pp; English.	
PS	The present invention relates to novel antisense oligonucleotides	
XX	(ACC71728-ACC71750 and ACC80101-ACC80155) targeted to Vascular	
CC	Endothelial Growth Factor Receptor-2 (VEGFR-2) nucleotide sequence, and	
CC	which inhibit the expression of VEGFR-2. The oligonucleotides are useful	
CC	in compositions for treating a disease or condition associated with VEGFR	
CC	-2, such as hyperproliferative disorder, e.g. cancer, a disease or	
CC	condition involving angiogenesis, or rheumatoid arthritis. The present	
CC	sequence is murine VEGFR-2	

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:30:47 ; Search time 19 Seconds  
(without alignments)  
3686.019 Million cell updates/sec

Title: US-10-090-183-6

Perfect score: 7046

Sequence: 1 MESKALLAVALWFCVETRAA.....KXVDAVAVHDSGTTLSPPV 1345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6998	99.3	1367	1 VGR2_MOUSE	P35918 mus musculus
2	6732	95.5	1343	1 VGR2_RAT	O08775 rattus norv
3	6124.5	86.9	1356	1 VGR2_HUMAN	P35968 homo sapien
4	4810.5	68.3	1348	1 VGR2_COTUA	P52583 coturnix co
5	2746.5	39.0	1363	1 VGR3_MOUSE	P35917 mus musculus
6	2694.5	38.2	1338	1 VGR1_HUMAN	P17948 h vascular
7	2677.5	38.0	1298	1 VGR3_HUMAN	P35916 homo sapien
8	2606	37.0	1336	1 VGR1_RAT	P53767 rattus norv
9	2575	36.5	1333	1 VGR1_MOUSE	P35969 mus musculus
10	1162.5	16.5	1088	1 PGDS_RAT	P20786 rattus norv
11	1162	16.5	1089	1 PGDS_HUMAN	P16234 homo sapien
12	1146	16.3	1089	1 PGDS_MOUSE	P26618 mus musculus
13	1130.5	16.0	1087	1 PGDS_XENLA	P26619 xenopus lae
14	1043.5	14.8	960	1 KIT_CHICK	O08156 gallus gall
15	1019.5	14.5	976	1 KIT_HUMAN	P10721 homo sapien
16	1019	14.5	1106	1 PGDR_HUMAN	P05619 homo sapien
17	1016.5	14.4	975	1 KIT_MOUSE	P05532 mus musculus
18	1013.5	14.4	978	1 KIT_CAPIH	O28317 capra hircu
19	1011	14.3	1097	1 PGDR_RAT	O05030 rattus norv
20	1009	14.3	977	1 KIT_BOVIN	P43481 bos taurus
21	1005	14.3	978	1 KIT_FELCA	Q28889 felis silve
22	1003	14.2	806	1 CEK2_CHICK	P18460 gallus gall
23	1002.5	14.2	819	1 FGR1_CHICK	P21804 gallus gall
24	1000.5	14.2	1098	1 PGDR_MOUSE	P05622 mus musculus
25	994	14.1	980	1 KPM5_FELCA	P13369 felis silve
26	992	14.1	821	1 FGR2_MOUSE	P21363 mus musculus
27	990.5	14.1	975	1 KPM5_HUMAN	O77333 homo sapien
28	990	14.1	975	1 KIT_CANFA	O97799 canis fami
29	986	14.0	822	1 FGR1_MOUSE	P16092 mus musculus
30	985	14.0	822	1 FGR1_HUMAN	P11362 homo sapien
31	984	14.0	821	1 FGR2_HUMAN	P21802 homo sapien
32	979	13.9	978	1 KPM5_FSVMD	P00545 feline sarc
33	976.5	13.9	812	1 FGR1_XENLA	P22182 xenopus lae

#### ALIGNMENTS

RESULT 1  
VGR2\_MOUSE  
ID VGR2\_MOUSE STANDARD; PRT; 1367 AA.  
AC P35918;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)  
DE (VGFRR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase  
DE 1) (Kinase NYK).  
GN KDR OR FLK1 OR FLK-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Embryo;  
EX MEDLINE=9320880; PubMed=7681362;  
RA Millauer B., Witzmann-Voos S., Schnurch H., Martinez R.,  
RA Mueller N.P.H., Risaue W., Ullrich A.;  
RT "High affinity VEGF binding and developmental expression suggest  
RT Flk-1 as a major regulator of vasculogenesis and angiogenesis.";  
RL Cell 72:835-846(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/He; TISSUE=Fetal liver;  
RX MEDLINE=92020984; PubMed=1717995;  
RA Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,  
RA Lemishcka I.R.;  
RT "A receptor tyrosine kinase cDNA isolated from a population of  
RT enriched primitive hematopoietic cells and exhibiting close genetic  
RT linkage to c-kit.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93141255; PubMed=8423988;  
RA Oelrichs R.B., Reid H.N., Bernard O., Ziemiecki A., Wilks A.F.;  
RT "NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from  
RT E10 embryonic neuroepithelium is expressed in endothelial cells of  
RT the developing embryo";  
RL Oncogene 8:11-18(1993).  
RN [4]  
RP SEQUENCE OF 1-15 FROM N.A.  
RX MEDLINE=96032749; PubMed=7559454;  
RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,  
RA Harber E.;  
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a  
RT receptor for vascular endothelial growth factor.";  
RL J. Biol. Chem. 270:23111-23118(1995).  
RN [5]  
RP FUNCTION.  
RX MEDLINE=93361481; PubMed=8356051;  
RA Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;  
RT "Fetal liver kinase 1 is a receptor for vascular endothelial growth  
RT factor and is selectively expressed in vascular endothelium.";



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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:33:52 ; Search time 51 Seconds  
(without alignments)  
8321.019 Million cell updates/sec

Title: US-10-090-183-6  
Perfect score: 7046  
Sequence: 1 MESKALLAVALWFCVETRAA.....KWDAAVHADSGTILRSPPV 1345

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rhodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7040	99.9	1345	11 Q8VCD0	Q8VCD0 mus musculus
2	2913	41.3	1379	13 P79701	P79701 coturnix co
3	2730.5	38.8	1363	11 Q91ZT1	Q91ZT1 rattus norv
4	2666	37.8	1363	4 Q86W07	Q86W07 homo sapien
5	2661.5	37.8	1298	4 Q86W08	Q86W08 homo sapien
6	2639.5	37.5	1327	13 Q8QHL3	Q8QHL3 gallus gall
7	2495.5	35.4	1301	13 Q8UW99	Q8UW99 brachydanio
8	2493	35.4	1302	13 Q8AXB3	Q8AXB3 brachydanio
9	2357.5	33.5	1173	13 Q9PTL0	Q9PTL0 brachydanio
10	2210.5	31.4	1092	11 Q91ZT0	Q91ZT0 rattus norv
11	1796	25.5	341	11 Q8CD05	Q8CD05 mus musculu
12	1322.5	18.8	346	13 Q42570	Q42570 xenopus lae
13	1172	16.6	287	13 Q42377	Q42377 brachydanio
14	1154.5	16.4	1078	13 Q8AXC8	Q8AXC8 fugu rubrip
15	1150	16.3	1089	11 Q7TSJ3	Q7TSJ3 mus musculu
16	1135	16.1	976	13 Q9W755	Q9W755 brachydanio

17	1135	16.1	1062	13 Q8AXC7	Q8AXC7 fugu rubrip
18	1134	16.1	976	13 Q8JFR5	Q8JFR5 brachydanio
19	1133.5	16.1	1087	13 Q7ZY71	Q7ZY71 xenopus lae
20	1132	16.1	1059	13 Q9DB49	Q9DB49 brachydanio
21	1128.5	16.0	453	11 Q9CW58	Q9CW58 mus musculu
22	1128	16.0	984	13 Q8AXC6	Q8AXC6 fugu rubrip
23	1114.5	15.8	1087	13 Q9PUF6	Q9PUF6 gallus gall
24	1097	15.6	207	6 Q9N112	Q9N112 ovis aries
25	1089	15.5	992	13 Q8AXU0	Q8AXU0 oncorhynch
26	1077.5	15.3	975	13 P79750	P79750 fugu rubrip
27	1075.5	15.3	1474	5 Q8T4M0	Q8T4M0 drosophila
28	1074	15.2	1503	5 Q8T4L8	Q8T4L8 drosophila
29	1065	15.1	1509	5 Q9SP10	Q9SP10 drosophila
30	1064	15.1	1509	5 Q8IPG1	Q8IPG1 drosophila
31	1049.5	14.9	1048	13 P79749	P79749 fugu rubrip
32	1049	14.9	1509	5 Q9VLQ8	Q9VLQ8 drosophila
33	1045	14.8	1461	5 Q8T9F6	Q8T9F6 drosophila
34	1040.5	14.8	977	13 Q98SU2	Q98SU2 dario kerri
35	1037.5	14.7	977	13 Q98SU4	Q98SU4 dario alboi
36	1037	14.7	974	13 Q98SU3	Q98SU3 dario dangi
37	1034.5	14.7	977	13 Q98SU1	Q98SU1 dario nigro
38	1033.5	14.7	977	13 Q918N6	Q918N6 brachydanio
39	1027.5	14.6	986	13 Q8UVR9	Q8UVR9 fugu rubrip
40	1026.5	14.6	979	11 Q8C8K9	Q8C8K9 mus musculu
41	1023.5	14.5	975	11 Q7TS86	Q7TS86 mus musculu
42	1023.5	14.5	1019	13 Q8UVR8	Q8UVR8 fugu rubrip
43	1023	14.5	445	5 Q9U8U8	Q9U8U8 brachiosco
44	1019	14.5	974	11 Q63702	Q63702 rattus ratt
45	1019	14.5	978	11 Q63116	Q63116 rattus norv

## ALIGNMENTS

### RESULT 1

ID	Q8VCD0	PRELIMINARY;	PRT; 1345 AA.
AC	Q8VCD0;		
DT	01-MAR-2002 (TREMREL. 20, Created)		
DT	01-MAR-2002 (TREMREL. 20, Last sequence update)		
DT	01-OCT-2003 (TREMREL. 25, Last annotation update)		
DE	Kinase insert domain protein receptor.		
GN	KDR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Strausberg R.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.		
DR	EMBL; BC020530; AAH20530.1; -.		
DR	MGP; MGI:96683; Kdr.		
DR	GO; GO:0045155; P:cell fate commitment; IMP.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR001824; RecepttyrknsIII.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	InterPro; IPR008266; Tyr_kinase_AS.		
DR	Pfam; PF00047; Ig; 6.		
DR	Pfam; PF00069; pkinase; 1.		
DR	ProDom; PD000001; Prot_kinase; 2.		
DR	SMART; SM00408; IGc2; 1.		
DR	SMART; SM00219; TyrKc; 1.		
DR	PROSITE; PS00835; IG-LIKE; 5.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		



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OW nucleic - nucleic search, using sw model

Run on: August 6, 2004, 15:55:08 / Search time 1541 Seconds  
(without alignments)  
17149.854 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtcccgaccgggata.....ctgtgctgtgcttatgtt 5390

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: Published Applications NA:

- 2: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
- 6: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
- 7: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq\*
- 9: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5390	100.0	5390	15	US-10-090-183-5
2	5346	99.2	5470	9	US-09-766-678-1
3	5346	99.2	5470	10	US-09-967-655-10
4	5336.8	99.0	5406	9	US-09-919-408-5
5	5336.8	99.0	5406	9	US-09-872-136-5
6	3356	62.3	5841	15	US-10-133-013-269
7	3354.4	62.2	5832	13	US-10-116-802-18
8	3317.8	61.6	5830	10	US-09-967-655-3
9	3317.8	61.6	5830	16	US-10-159-563-338
10	3317.8	61.6	5830	16	US-10-294-228-7
11	3050.8	56.8	4230	15	US-10-262-538-29
12	3027.8	56.2	4071	15	US-10-327-414-5
13	3027.8	56.2	4071	15	US-10-090-183-1
14	3024.6	56.1	4071	15	US-10-022-939-1
15	3024.6	56.1	4071	15	US-10-090-183-5

15	3024.6	56.1	4071	15	US-10-100-405A-1	Sequence 1, Appl
16	2412.4	44.8	2431	14	US-10-036-869-35	Sequence 35, Appl
17	2271	42.1	2271	15	US-10-364-949-1	Sequence 1, Appl
18	1656.8	30.7	2383	15	US-10-101-018-18	Sequence 18, Appl
19	1609.2	29.9	2320	15	US-10-364-949-3	Sequence 3, Appl
20	1601.2	29.7	2351	15	US-10-091-300-84	Sequence 84, Appl
21	1420	26.3	2264	15	US-10-101-018-16	Sequence 16, Appl
22	1374.8	25.5	1704	15	US-10-327-414-7	Sequence 7, Appl
23	768	14.2	4017	15	US-10-090-183-3	Sequence 3, Appl
24	768	14.2	7680	10	US-09-953-318-3	Sequence 3, Appl
25	768	14.2	7680	13	US-10-211-462-214	Sequence 214, App
26	768	14.2	7680	13	US-10-342-887-711	Sequence 711, App
27	768	14.2	7680	13	US-10-172-118-711	Sequence 711, App
28	768	14.2	7680	13	US-10-446-373-3	Sequence 3, Appl
29	768	14.2	7680	13	US-10-021-660-16	Sequence 16, Appl
30	768	14.2	7680	15	US-10-393-590-77	Sequence 77, Appl
31	768	14.2	7680	15	US-10-393-567-77	Sequence 77, Appl
32	768	14.2	7680	15	US-10-394-087-77	Sequence 25, Appl
33	768	14.2	7680	17	US-10-621-116-25	Sequence 1, Appl
34	716.2	13.3	4111	10	US-09-375-248-1	Sequence 1, Appl
35	716.2	13.3	4111	13	US-10-661-740-1	Sequence 1, Appl
36	716.2	13.3	4195	13	US-09-765-534B-1	Sequence 31, Appl
37	716.2	13.3	4195	15	US-10-262-538-31	Sequence 1, Appl
38	716.2	13.3	4195	15	US-10-201-386-1	Sequence 31, Appl
39	716.2	13.3	4425	9	US-09-982-610-31	Sequence 31, Appl
40	716.2	13.3	4425	17	US-10-641-643-889	Sequence 889, App
41	716.2	13.3	4795	13	US-09-765-534B-3	Sequence 3, Appl
42	716.2	13.3	9108	9	US-09-982-610-45	Sequence 45, Appl
43	710.2	13.2	4113	15	US-10-081-126-1	Sequence 1, Appl
44	710.2	13.2	4450	17	US-10-326-048-3	Sequence 3, Appl
45	694.4	12.9	6055	10	US-09-953-318-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
US-10-090-183-5  
; Sequence 5, Application US/10090183  
; Publication No. US20030185802A1  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Ralph A. Reisfeld  
; APPLICANT: Andrew G. Niethammer  
; APPLICANT: Rong Xiang  
; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING  
; TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF  
; FILE REFERENCE: TSRI-829.0  
; CURRENT APPLICATION NUMBER: US/10/090,183  
; CURRENT FILING DATE: 2002-03-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 5390  
; TYPE: DNA  
; ORGANISM: mouse  
US-10-090-183-5

Query Match	100.0%	Score 5390;	DB 15;	Length 5390;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 5390;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	CTGTGTCCCGCAGCCGGATTAACCTGCTGACCCGGATTCCCGGACACCGCTGCAGCCGCG	60	
Db	1	CTGTGTCCCGCAGCCGGATTAACCTGCTGACCCGGATTCCCGGACACCGCTGCAGCCGCG	60	
Qy	61	GCTGTGAGCAGCGCGCGCGGTGCCCCCGGCTCTCCCGGCTTTCGCTGCGGGGCCATAC	120	
Db	61	GCTGTGAGCAGCGCGCGCGGTGCCCCCGGCTCTCCCGGCTTTCGCTGCGGGGCCATAC	120	
Qy	121	CGCTCTGTGACTTCTTTTGGGGCCAGGAGGAGTCTGTGCTGAGAACTGG	180	
Db	121	CGCTCTGTGACTTCTTTTGGGGCCAGGAGGAGTCTGTGCTGAGAACTGG	180	



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	5346	99.2	5470	2	US-08-443-861-1	Sequence 1, Appli
2	5346	99.2	5470	3	US-08-193-8298-1	Sequence 1, Appli
3	5336.8	99.0	5406	1	US-07-813-593-3	Sequence 3, Appli
4	5336.8	99.0	5406	1	US-07-977-451-5	Sequence 3, Appli
5	5336.8	99.0	5406	1	US-07-946-507-3	Sequence 3, Appli
6	5336.8	99.0	5406	1	US-08-252-517-5	Sequence 5, Appli
7	5336.8	99.0	5406	1	US-07-906-397A-5	Sequence 5, Appli
8	5336.8	99.0	5406	1	US-08-601-891-5	Sequence 5, Appli
9	5336.8	99.0	5406	2	US-09-021-324-5	Sequence 5, Appli
10	5336.8	99.0	5406	1	US-09-872-136B-5	Sequence 5, Appli
11	5336.8	99.0	5406	5	PCT-US92-02750-7	Sequence 7, Appli
12	5336.8	99.0	5406	5	PCT-US92-05401-5	Sequence 5, Appli
13	5336.8	99.0	5406	5	PCT-US92-09893-5	Sequence 5, Appli
14	3066.8	56.9	4236	1	US-08-810-116-7	Sequence 7, Appli
15	3066.8	56.9	4236	2	US-07-930-548A-7	Sequence 7, Appli
16	3024.6	56.1	4071	3	US-09-098-707A-1	Sequence 1, Appli
17	3024.6	56.1	4071	4	US-09-483-539-1	Sequence 1, Appli
18	2412.4	44.8	2431	3	US-08-985-526-35	Sequence 35, Appli
19	1656.8	30.7	2383	1	US-08-232-538-18	Sequence 18, Appli
20	1656.8	30.7	2383	2	US-08-786-164-18	Sequence 18, Appli
21	1592.4	29.5	2292	4	US-09-142-956B-1	Sequence 1, Appli
22	1420	26.3	2264	1	US-08-232-538-16	Sequence 16, Appli
23	1420	26.3	2264	2	US-08-786-164-16	Sequence 16, Appli
24	768	14.2	4014	4	US-09-119-014D-5	Sequence 5, Appli
25	757	14.0	7718	4	US-09-976-594-244	Sequence 244, App
26	716.2	13.3	4195	1	US-08-340-011-1	Sequence 1, Appli
27	716.2	13.3	4195	3	US-08-903-710-1	Sequence 1, Appli

Result No.	Score	Query Match	Length	DB ID	Description
1	2106.6	39.1	2612	11	AK031739
2	1566.8	29.1	3176	11	AK054510
3	816.2	15.1	868	14	CA979203
4	765.6	14.2	809	13	BU709245
					UI-N-EVO-
					BU709245
					CA979203
					AGENCOURT
					AK054510
					Mus muscu
					AK031739
					Mus muscu

REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu N., Sugahara Y., Shibata, K., Itoh M, Konno, H, Okazaki Y, Muramatsu M and Hayashizaki Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 1229 Seconds  
(without alignments)

18631.235 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtccgcagccggata.....tctgctgtgtgttatgctt 5390

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_23Jan04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002s.\*

7: Geneseqn2003as.\*

8: Geneseqn2003bs.\*

9: Geneseqn2003cs.\*

10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5390	100.0	5390	9	ACF80603 Murine fl
2	5346	99.2	5470	7	ACC71720 Murine va
3	5336.8	99.0	5406	2	AAQ40916 Murine fl
4	5336.8	99.0	5406	2	AAQ53504 Murine fl
5	5336.8	99.0	5406	2	AAQ79070 Mouse flk
6	5336.8	99.0	5406	2	AAQ81014 Flk1 rece
7	5336.8	99.0	5406	2	AAT72119 Murine fl
8	5336.8	99.0	5406	6	AB555046 Mouse cDN
9	5335.2	99.0	5406	2	AAQ35251 Human flk
10	5331.6	98.9	5470	2	AAQ64049 Sequence
11	5330.4	98.9	5406	2	AAQ29957 flk-1 cDN
12	5322.8	98.8	5404	2	AAT38735 Murine fo
13	5322.8	98.8	5404	2	AAT77516 Murine fl
14	5074.8	94.2	5363	6	AAQ42485 Murine re
15	4259	79.0	5892	9	ADB58183 Toxicity-
16	3354.4	62.2	5832	8	ACH03813 Human cDN
17	3317.8	61.6	5830	7	ACC71713 Human vas
18	3316.2	61.5	5830	9	ADD08953 Human VEG
19	3081.2	57.2	4225	4	AAQ83308 Human VEG
20	3066.8	56.9	4236	2	AAV34763 Human KDR
21	3027.8	56.2	4071	6	ABV78213 Human KDR
22	3027.8	56.2	4071	6	AB35789 Human KDR
23	3027.8	56.2	4071	6	ABX10032 Human KDR

#### ALIGNMENTS

RESULT 1  
ACF80603

ID ACF80603 standard; cDNA, 5390 BP.

XX AC ACF80603;

XX DT 15-JAN-2004 (first entry)

XX DE Murine Flk-1 coding sequence.

XX KW Mouse; vascular endothelial growth factor; receptor; Flk-1; vaccine;

XX KW genetic immunisation; gene therapy; cytostatic; gene; ss.

XX OS Mus sp.

XX XX

XX FH Key Location/Qualifiers

XX CDS 208..4347

XX FT /\*tag= a

XX FT /product= "Mouse Flk-1"

XX PN WO2003073995-A2.

XX PD 12-SEP-2003.

XX PF 28-FEB-2003; 2003WO-US006256.

XX PR 02-MAR-2002; 2002US-00090183.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Reisfeld RA, Niethammer AG, Xiang R;

XX XX WPI; 2003-756753/71.

XX DR P-PSDB; ABM79009.

XX XX

XX PT New DNA vaccine for eliciting an immune response against proliferating

XX PT endothelial cells comprising a DNA construct operably encoding a VEGF

XX PT receptor protein in a carrier, useful for inhibiting tumor growth or

XX PS angiogenesis.

XX XX Claim 9; Fig 5; 56pp; English.

XX XX

XX CC The present sequence is the coding sequence for murine Flk-1, an

XX CC endothelial growth factor receptor protein. A claimed DNA vaccine

XX CC effective for eliciting an immune response against proliferating

XX CC endothelial cells comprises a DNA construct operably encoding a VEGF

Ab191754 Human pol  
Acf80601 Human VEG  
Abv78210 Human Flk  
Abz35786 Human Flk  
Abx10029 Human Flk  
Ab191751 Human pol  
Aaq28272 A novel c  
Aav99829 Human rec  
Aax58739 DNA encod  
Adb80299 DNA encod  
Aat95837 DNA for v  
Aaq74276 Truncated  
Aav9332 Soluble c  
Aax04434 Human sol  
Aaa91132 Flk-1extr  
Adb80301 DNA encod  
Aad46306 Human DNA  
Abt23341 VEGF bind  
Add44477 Human ant  
Add80854 Human KDR  
Aav50368 KDR codin  
Aaf83310 Human VEG

CC receptor protein (e.g. Flk-1) in a carrier. The DNA construct may be a  
 CC naked DNA construct or incorporated into a plasmid vector or into an  
 CC attenuated bacterial vector such as attenuated *Salmonella typhimurium*.  
 CC The DNA vaccine is used in claimed methods of inhibiting endothelial cell  
 CC proliferation, inhibiting angiogenesis, and inhibiting tumour growth  
 XX  
 SQ Sequence 5390 BP; 1397 A; 1297 C; 1422 G; 1274 T; 0 U; 0 Other;

Query Match		100.0%; Score 5390; DB 9; Length 5390;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 5390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	CTGTGTCCTCCGACGCGGATACCTGGCTGACCGGATTCGGCGGACACCGCTGCGACCGCG 60
Db	1	CTGTGTCCTCCGACGCGGATACCTGGCTGACCGGATTCGGCGGACACCGCTGCGACCGCG 60
Qy	61	GCTGGACCGACGCGGCTGCTCCCGCTCTCCCGCTCTGCGCTGCGCGGCGGCGATAC 120
Db	61	GCTGGACCGACGCGGCTGCTCCCGCTCTCCCGCTCTGCGCTGCGCGGCGGCGATAC 120
Qy	121	CGCTCTGTGACTTCTTTGGGCGGACGAGAGAGAGTCTGCTGAGAAACTGG 180
Db	121	CGCTCTGTGACTTCTTTGGGCGGACGAGAGAGAGTCTGCTGAGAAACTGG 180
Qy	181	GCTCTGTGCGGACGCGGAGTGCAGATGAGAGAGAGAGTCTGCTGAGAAACTGG 180
Db	181	GCTCTGTGCGGACGCGGAGTGCAGATGAGAGAGAGAGTCTGCTGAGAAACTGG 180
Qy	241	TGGTTCTGTGAGACCGGACGCGCTCTGTGGGTTTGAATGCGGATTTCTCCATCCC 300
Db	241	TGGTTCTGTGAGACCGGACGCGCTCTGTGGGTTTGAATGCGGATTTCTCCATCCC 300
Qy	301	CCCAAGCTCAGCACACAGAAACATCTGACAAATTTGGCAATAACAACCTTCAGATT 360
Db	301	CCCAAGCTCAGCACACAGAAACATCTGACAAATTTGGCAATAACAACCTTCAGATT 360
Qy	361	ACTTGACGGGACAGCGGACCTGACCTGGCTTGGCCCAATGCTCAGGTGATTCGAG 420
Db	361	ACTTGACGGGACAGCGGACCTGACCTGGCTTGGCCCAATGCTCAGGTGATTCGAG 420
Qy	421	GAAAGGTTATGCTGAATGCGGCGGTGTGACAGTATCTCTGCAAAACACTCACC 480
Db	421	GAAAGGTTATGCTGAATGCGGCGGTGTGACAGTATCTCTGCAAAACACTCACC 480
Qy	481	ATTCACAGGTTGGAATGATCTGAGGCTTACAGTCTGCTGACCGGAGCTGAC 540
Db	481	ATTCACAGGTTGGAATGATCTGAGGCTTACAGTCTGCTGACCGGAGCTGAC 540
Qy	541	ATAGCTTCCACTGTTATGCTATGTTGAGATTTACAGATCACCATTGCTCTGTC 600
Db	541	ATAGCTTCCACTGTTATGCTATGTTGAGATTTACAGATCACCATTGCTCTGTC 600
Qy	601	AGTGACAGCATGCGATCGTGTATCATCCAGAGAAACAGAAACAACTGTTGATCCCC 660
Db	601	AGTGACAGCATGCGATCGTGTATCATCCAGAGAAACAGAAACAACTGTTGATCCCC 660
Qy	661	TGCGGAGGTTGGAATTTCAACCTCAATGTCTCTTTGCGTAGTATCCAGAAAGAGA 720
Db	661	TGCGGAGGTTGGAATTTCAACCTCAATGTCTCTTTGCGTAGTATCCAGAAAGAGA 720
Qy	721	TTTGTTCGAGTGAACAGAAATTTCTGGGACGAGCATAGGCTTTTCTCCCACT 780
Db	721	TTTGTTCGAGTGAACAGAAATTTCTGGGACGAGCATAGGCTTTTCTCCCACT 780
Qy	781	TACATGATCAGCTATGCGGCTATGCTCTCTGTGAGGCAAGATCAATGAAACCTAT 840
Db	781	TACATGATCAGCTATGCGGCTATGCTCTCTGTGAGGCAAGATCAATGAAACCTAT 840
Qy	841	CAGTCTATCATGATAGTGTGTTGATATAGGATTTATGATGATTTCTGAGC 900
Db	841	CAGTCTATCATGATAGTGTGTTGATATAGGATTTATGATGATTTCTGAGC 900
Qy	901	CCCCGCAATGAATGAGCTATCTGCGGAGAAACCTTGCTTTAAATTTGTACAGCGAGA 960

Db	901	CCCCGCAATGAATGAGCTATCTGCGGAGAAACCTTGCTTTAAATTTGTACAGCGAGA 960
Qy	961	ACAGAGCTCAATGTGGGCTTGATTTACCTGGCACTCTCCACCTTCAAGTCTCATCAT 1020
Db	961	ACAGAGCTCAATGTGGGCTTGATTTACCTGGCACTCTCCACCTTCAAGTCTCATCAT 1020
Qy	1021	AAGAAGATTGTAAACCGGGATGTGAAACCTTCTCTGGCACTGTGGCGAAGATTTTGG 1080
Db	1021	AAGAAGATTGTAAACCGGGATGTGAAACCTTCTCTGGCACTGTGGCGAAGATTTTGG 1080
Qy	1081	AGCACTTGTGACATAGAAAGTGTGACCAAGAGTGCACCAAGGGGATATACACCTGTGTAGCG 1140
Db	1081	AGCACTTGTGACATAGAAAGTGTGACCAAGAGTGCACCAAGGGGATATACACCTGTGTAGCG 1140
Qy	1141	TCCAGTGGACGCGATGATCAAGAGAAATAGAAATTTGTCTCGAGTTTCAACAAGCCCTTTT 1200
Db	1141	TCCAGTGGACGCGATGATCAAGAGAAATAGAAATTTGTCTCGAGTTTCAACAAGCCCTTTT 1200
Qy	1201	ATTGCTTTTCCGTAGTGGGATGAAATCTTTGGTGGAGGCCACAGTGGGCACTCAAGTCCGA 1260
Db	1201	ATTGCTTTTCCGTAGTGGGATGAAATCTTTGGTGGAGGCCACAGTGGGCACTCAAGTCCGA 1260
Qy	1261	ATCCCTGTGCAAGTATCTCAGTTACCCAGCTCTCTGATATCAAAATGGTACAGAAATGGAAG 1320
Db	1261	ATCCCTGTGCAAGTATCTCAGTTACCCAGCTCTCTGATATCAAAATGGTACAGAAATGGAAG 1320
Qy	1321	CCCATTTAGTCCAACTACACATGATTTGGCGATGAATCAACATCATGGAAGTGAAT 1380
Db	1321	CCCATTTAGTCCAACTACACATGATTTGGCGATGAATCAACATCATGGAAGTGAAT 1380
Qy	1381	GAAAGAGATGACAGGAACTACACGCTCATCTTCCACCAACCCCATTTCAATGAGAAACAG 1440
Db	1381	GAAAGAGATGACAGGAACTACACGCTCATCTTCCACCAACCCCATTTCAATGAGAAACAG 1440
Qy	1441	AGCCACATGCTCTCTGTTGTGAATGTCCTCCACCCAGATCGGTGAGAAAGCCCTTGATC 1500
Db	1441	AGCCACATGCTCTCTGTTGTGAATGTCCTCCACCCAGATCGGTGAGAAAGCCCTTGATC 1500
Qy	1501	TGCGCTATGATTCCTACCACTATGGGACCATGACAGATTCAGATGACATGACATGACGCT 1560
Db	1501	TGCGCTATGATTCCTACCACTATGGGACCATGACAGATTCAGATGACATGACATGACGCT 1560
Qy	1561	AACCTTCCCTGACCACTCAGTGTGTACTGGCAGCTAGAGAGCTGCTGCTCTACAGA 1620
Db	1561	AACCTTCCCTGACCACTCAGTGTGTACTGGCAGCTAGAGAGCTGCTGCTCTACAGA 1620
Qy	1621	CCCGGCCAAACAGCCGTTATGCTTTAAAGATGGAGACACGTTGAGGATTTCCAGGGG 1680
Db	1621	CCCGGCCAAACAGCCGTTATGCTTTAAAGATGGAGACACGTTGAGGATTTCCAGGGG 1680
Qy	1681	GGAAACAGATGCAAGTCAACCAACCAATATGCTTCAATGAGGATTTTCAAGAACT 1740
Db	1681	GGAAACAGATGCAAGTCAACCAACCAATATGCTTCAATGAGGATTTTCAAGAACT 1740
Qy	1741	GTAAGTACGCTGCTCATCCAGCTGCAACGCTGACGCTTGTACAAATGTGAAGCAATC 1800
Db	1741	GTAAGTACGCTGCTCATCCAGCTGCAACGCTGACGCTTGTACAAATGTGAAGCAATC 1800
Qy	1801	ACCAAGCGGACGAGGAGAGAGGCTCATCTCTTCCATGCTATCAGGCTCTCTGAAAT 1860
Db	1801	ACCAAGCGGACGAGGAGAGAGGCTCATCTCTTCCATGCTATCAGGCTCTCTGAAAT 1860
Qy	1861	ACTGTGCAACTGCTGCGGACGAGAGAGGCTCATCTCTTCCATGCTATCAGGCTCTCTGAAAT 1920
Db	1861	ACTGTGCAACTGCTGCGGACGAGAGAGGCTCATCTCTTCCATGCTATCAGGCTCTCTGAAAT 1920
Qy	1921	GACAGAAATACGTTTGAAGAACTCAGCTGCTGACAGCTTGGCTCAGGCAACATCGGTC 1980
Db	1921	GACAGAAATACGTTTGAAGAACTCAGCTGCTGACAGCTTGGCTCAGGCAACATCGGTC 1980
Qy	1981	CACATGGCGAATCACTCACAACAGTTTGAAGAACTTGGATGCTCTTTTGAAGCTGAAT 2040

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 13494 Seconds  
(without alignments)  
17312.802 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtccgcagccggata.....ctgctgtgtgcttatgtt 5390

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_or.\*

21: em\_ov.\*

22: em\_pat.\*

23: em\_ph.\*

24: em\_pl.\*

25: em\_ro.\*

26: em\_sts.\*

27: em\_un.\*

28: em\_vl.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_ey.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5366.2	99.6	5391	10 MMFLK1	X59397 Mouse Plk-1
2	5346	99.2	5470	6 AR068047	AR068047 Sequence
3	5346	99.2	5470	6 AR125598	AR125598 Sequence
4	5346	99.2	5470	10 MMFLK1M	X70842 M.musculus
5	5336.8	99.0	5406	6 AR005213	AR005213 Sequence
6	5336.8	99.0	5406	6 AR071705	AR071705 Sequence
7	5336.8	99.0	5406	6 I25171	I25171 Sequence 5
8	5336.8	99.0	5406	6 I40602	I40602 Sequence 5
9	5279.6	98.0	5464	10 BC020530	BC020530 Mus muscu
10	4657.2	86.4	4790	10 S53103	S53103 NYK/PLK-1
11	4259	79.0	5892	10 RNU93306	RNU93306 Rattus norv
12	3317.8	61.6	5830	6 AX743112	AX743112 Sequence
13	3317.8	61.6	5830	9 AF035121	AF035121 Homo sapi
14	3081.2	57.2	4225	6 AX133539	AX133539 Sequence
15	3066.8	56.9	4236	6 AR030758	AR030758 Sequence
16	3060.8	56.8	4230	9 HSGPRTK	X61656 H.sapiens m
17	3060.8	56.8	4230	9 HUMKDRZ	L04947 Homo sapien
18	3027.8	56.2	4071	6 AX481483	AX481483 Sequence
19	3027.8	56.2	4071	9 AF063658	AF063658 Homo sapi
20	3026.2	56.1	4044	6 AX481480	AX481480 Sequence
21	3024.6	56.1	4071	6 AR142803	AR142803 Sequence
22	3024.6	56.1	4071	6 AR201382	AR201382 Sequence
23	3024.6	56.1	4071	6 BD132942	BD132942 Human rec
24	2728	50.6	4016	10 RNU93307	RNU93307 Rattus norv
25	2412.4	44.8	2431	6 AR100641	AR100641 Sequence
26	2412.4	44.8	2431	6 E34072	E34072 Carrier/DNA
27	1904.8	35.3	5390	5 CCQUEK1	X83288 C.cotturrix
28	1753.8	32.5	2555	6 A64406	A64406 Sequence 19
29	1656.8	30.7	2383	6 AR030850	AR030850 Sequence
30	1656.8	30.7	2383	6 I82809	I82809 Sequence 18
31	1621.6	30.1	3009	6 AX060542	AX060542 Sequence
32	1592.4	29.5	2292	6 AR194072	AR194072 Sequence
33	1581.4	29.3	2281	6 AX133543	AX133543 Sequence
34	1420	26.3	2264	6 AR030848	AR030848 Sequence
35	1420	26.3	2264	6 I82807	I82807 Sequence 16
36	1279.2	23.7	221665	2 AC134903	AC134903 Mus muscu
37	810.6	15.0	4617	5 CCQUEK2	X83287 C.cotturrix
38	768	14.2	4014	6 AR397397	AR397397 Sequence
39	768	14.2	4017	6 AX481481	AX481481 Sequence
40	768	14.2	4017	9 AF063657	AF063657 Homo sapi
41	768	14.2	7680	9 HSFLT	X51602 Human flt m
42	727.8	13.5	2619	5 S65205	S65205 endothelial
43	727	13.5	4272	5 AB065372	AB065372 Gallus ga
44	720.6	13.4	5284	10 MUSRTKA	L07296 Mus musculu
45	717.8	13.3	3897	6 AX481482	AX481482 Sequence

#### ALIGNMENTS

RESULT 1

MMFLK1

LOCUS

DEFINITION Mouse Plk-1 mRNA for a tyrosine kinase receptor.

ACCESSION X59397

VERSION X59397.1 GI:50976

KEYWORDS Plk-1 gene; tyrosine kinase receptor.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 5391)

AUTHORS Matthews,W., Jordan,C.T., Gavin,M., Jenkins,N.A., Copeland,N.G. and Lemischka,I.R.

TITLE

A receptor tyrosine kinase cDNA isolated from a population of